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RAW SEQUENCE LISTING   DATE: 07/23/2002 P.6
PATENT APPLICATION: US/10/086,464   TIME: 13:08:23

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\07232002\J086464.raw

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 4 <110> APPLICANT: GORING, Daphne R. et al.
 6 <120> TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
 8 <130> FILE REFERENCE: P 25,762-A USA
10 <140> CURRENT APPLICATION NUMBER: US 10/086,464
11 <141> CURRENT FILING DATE: 2002-02-28
13 <150> PRIOR APPLICATION NUMBER: US 10/069,304
14 <151> PRIOR FILING DATE: 2002-02-19
16 <150> PRIOR APPLICATION NUMBER: PCT/CA00/00966
17 <151> PRIOR FILING DATE: 2000-08-18
19 <150> PRIOR APPLICATION NUMBER: US 60/149,466
20 <151> PRIOR FILING DATE: 1999-08-19
22 <150> PRIOR APPLICATION NUMBER: US 60/159,122
23 <151> PRIOR FILING DATE: 1999-10-13
25 <160> NUMBER OF SEQ ID NOS: 27
27 <170> SOFTWARE: PatentIn Ver. 2.1
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1944
31 <212> TYPE: DNA
32 <213> ORGANISM: Brassica napus
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35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)..(1944)
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43 tca aac tcc aca acc acc act cct cct cca gct tcc gct cct cct ccc   96
44 Ser Asn Ser Thr Thr Thr Thr Pro Pro Pro Ala Ser Ala Pro Pro Pro
45                  20                  25                  30
47 acc aca cct tct tct cct ccg ccg cca tcc act att ccg aca tct cct  144
48 Thr Thr Pro Ser Ser Pro Pro Pro Pro Ser Thr Ile Pro Thr Ser Pro
49              35                  40                  45
51 cct cct tct tct cgc tct aca cct tct gct cct cct cca tct cca cca  192
52 Pro Pro Ser Ser Arg Ser Thr Pro Ser Ala Pro Pro Pro Ser Pro Pro
53          50                  55                  60
55 act cca tct acg ccg gga tct cca cct cct ctt cct cag ccg tct cca  240
56 Thr Pro Ser Thr Pro Gly Ser Pro Pro Pro Leu Pro Gln Pro Ser Pro
57 65                   70                  75                  80
59 ccc gct cca act acg ccc gga tct cca ccc gca cct gtt act cct cct  288
60 Pro Ala Pro Thr Thr Pro Gly Ser Pro Pro Ala Pro Val Thr Pro Pro
61                  85                  90                  95
63 act cga aac cct cca cct tca gtc cca gga cca ccg tcc aat cct tca  336
64 Thr Arg Asn Pro Pro Pro Ser Val Pro Gly Pro Pro Ser Asn Pro Ser
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/086,464

DATE: 07/23/2002
TIME: 13:08:23

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\07232002\J086464.raw

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65              100              105              110
67 cgc gaa gga gga tct cct cga cct cca tct tct ccc tcg ccg ccg tct   384
68 Arg Glu Gly Gly Ser Pro Arg Pro Pro Ser Ser Pro Ser Pro Pro Ser
69         115              120              125
71 cct tct tcc gac ggt tta tca aca gga gtg gtg gtg gga atc gcc atc   432
72 Pro Ser Ser Asp Gly Leu Ser Thr Gly Val Val Val Gly Ile Ala Ile
73     130              135              140
75 gga gga gtc gct ctg ctt gtg ata gtg act ctg att tgt ctc ctc tgt   480
76 Gly Gly Val Ala Leu Leu Val Ile Val Thr Leu Ile Cys Leu Leu Cys
77 145              150              155              160
79 aag aag aaa cga cgg aga gac gaa gaa gat gct tac tat gtt cct ccg   528
80 Lys Lys Lys Arg Arg Arg Asp Glu Glu Asp Ala Tyr Tyr Val Pro Pro
81              165              170              175
83 cca cct cct cct ggt ccc aaa gcc gga gga cct tac ggt gga cag cag   576
84 Pro Pro Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln
85         180              185              190
87 caa caa tgg cgg caa caa aac gca aca cca ccg tca gat cat gtc gtg   624
88 Gln Gln Trp Arg Gln Gln Asn Ala Thr Pro Pro Ser Asp His Val Val
89         195              200              205
91 acg tca cta cca cca cca cct aag gct cca tct cca cca cgg caa cct   672
92 Thr Ser Leu Pro Pro Pro Pro Lys Ala Pro Ser Pro Pro Arg Gln Pro
93     210              215              220
95 cct cca cct cca cca ccg cct ttc atg agc agc agc ggc ggc tcc gac   720
96 Pro Pro Pro Pro Pro Pro Pro Phe Met Ser Ser Ser Gly Gly Ser Asp
97 225              230              235              240
99 tac tcg gac cgt cca gtt ctt cct cca ccg tct cca ggg ctt gtg tta   768
100 Tyr Ser Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu
101              245              250              255
103 ggc ttc tcc aaa agc act ttc aca tac gag gag cta gct aga gcc acc   816
104 Gly Phe Ser Lys Ser Thr Phe Thr Tyr Glu Glu Leu Ala Arg Ala Thr
105         260              265              270
107 aat ggt ttc tcc gag gcg aac ttg tta gga caa ggc ggg ttc ggt tac   864
108 Asn Gly Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr
109         275              280              285
111 gtg cac aaa ggt gtg ttg cct agt ggg aaa gaa gtt gct gtg aag cag   912
112 Val His Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln
113     290              295              300
115 ttg aaa gtt ggg agt ggt cag gga gag agg gag ttt cag gca gag gtt   960
116 Leu Lys Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val
117 305              310              315              320
119 gag atc atc agc aga gtt cac cac agg cat ctg gtg tct ctt gtt ggt   1008
120 Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly
121              325              330              335
123 tat tgc atc gcc ggt gcc aaa aga ttg ctt gtc tat gag ttt gtt cct   1056
124 Tyr Cys Ile Ala Gly Ala Lys Arg Leu Leu Val Tyr Glu Phe Val Pro
125         340              345              350
127 aac aac aat ctc gag ctt cac ctc cat ggc gag gga cgg cct aca atg   1104
128 Asn Asn Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met
129         355              360              365
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RAW SEQUENCE LISTING   DATE: 07/23/2002
PATENT APPLICATION: US/10/086,464   TIME: 13:08:23

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\07232002\J086464.raw

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131 gaa tgg agc acc aga ttg aag att gct ctt gga tct gct aaa gga ctt   1152
132 Glu Trp Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu
133     370             375             380
135 tct tat ctt cat gaa gat tgc aat cct aaa atc att cac cgt gat atc   1200
136 Ser Tyr Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile
137 385             390             395             400
139 aag gct tca aac ata ttg ata gat ttc aag ttt gaa gct aag gtt gct   1248
140 Lys Ala Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala
141             405             410             415
143 gat ttt ggt ctt gct aag att gct tct gat aca aac acg cat gta tca   1296
144 Asp Phe Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser
145             420             425             430
147 aca cgt gtg atg gga acc ttt ggg tac ttg gct ccg gaa tac gct gca   1344
148 Thr Arg Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala
149             435             440             445
151 agc gga aag ctc acg gag aag tct gac gtt ttc tca ttt ggc gtt gtg   1392
152 Ser Gly Lys Leu Thr Glu Lys Ser Asp Val Phe Ser Phe Gly Val Val
153     450             455             460
155 ctt ttg gag ctc att act gga cgt cga ccc gtt gat gcc aac aat gtc   1440
156 Leu Leu Glu Leu Ile Thr Gly Arg Arg Pro Val Asp Ala Asn Asn Val
157 465             470             475             480
159 tat gta gat gac agc tta gtt gac tgg gca cga cca ttg ctt aac cga   1488
160 Tyr Val Asp Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Leu Asn Arg
161             485             490             495
163 gca tct gag caa gga gac ttt gag ggt tta gct gat gca aag atg aat   1536
164 Ala Ser Glu Gln Gly Asp Phe Glu Gly Leu Ala Asp Ala Lys Met Asn
165             500             505             510
167 aat ggg tat gac aga gag gag atg gct cgc atg gtt gct tgt gct gcg   1584
168 Asn Gly Tyr Asp Arg Glu Glu Met Ala Arg Met Val Ala Cys Ala Ala
169     515             520             525
171 gct tgt gtt cgc cat tca gct cgc cgc aga cct cgc atg agc cag att   1632
172 Ala Cys Val Arg His Ser Ala Arg Arg Arg Pro Arg Met Ser Gln Ile
173     530             535             540
175 gtg cgt gcg tta gaa gga aat gta tca ctg tca gat ctt aac gaa ggg   1680
176 Val Arg Ala Leu Glu Gly Asn Val Ser Leu Ser Asp Leu Asn Glu Gly
177 545             550             555             560
179 atg aga cca ggt caa agc aat gta tac agc tca tac gga gga agc acc   1728
180 Met Arg Pro Gly Gln Ser Asn Val Tyr Ser Ser Tyr Gly Gly Ser Thr
181             565             570             575
183 gat tat gac tcg agc cag tac aat gaa gac atg aag aag ttt agg aaa   1776
184 Asp Tyr Asp Ser Ser Gln Tyr Asn Glu Asp Met Lys Lys Phe Arg Lys
185             580             585             590
186 atg gca ctt gga act caa gag tac aac gcc acg ggt gag tac agt aat   1824
187 Met Ala Leu Gly Thr Gln Glu Tyr Asn Ala Thr Gly Glu Tyr Ser Asn
188             595             600             605
190 ccg acc agt gac tat gga ctg tac ccg tct ggt tca agc agc gag ggc   1872
191 Pro Thr Ser Asp Tyr Gly Leu Tyr Pro Ser Gly Ser Ser Ser Glu Gly
192     610             615             620
194 caa acc aca cgc gaa atg gag atg ggg aag att aag aga acc ggt cag   1920
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195 Gln Thr Thr Arg Glu Met Glu Met Gly Lys Ile Lys Arg Thr Gly Gln
196 625               630               635               640
198 ggt tat agt gga cct tct ctt taa                                      1944
199 Gly Tyr Ser Gly Pro Ser Leu
200               645
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 647
205 <212> TYPE: PRT
206 <213> ORGANISM: Brassica napus
208 <400> SEQUENCE: 2
209 Met Ser Ser Ala Pro Ser Pro Gly Thr Gly Ser Pro Pro Ser Pro Pro
210  1               5               10               15
211 Ser Asn Ser Thr Thr Thr Thr Pro Pro Pro Ala Ser Ala Pro Pro Pro
212               20               25               30
213 Thr Thr Pro Ser Ser Pro Pro Pro Pro Ser Thr Ile Pro Thr Ser Pro
214               35               40               45
215 Pro Pro Ser Ser Arg Ser Thr Pro Ser Ala Pro Pro Pro Ser Pro Pro
216       50               55               60
217 Thr Pro Ser Thr Pro Gly Ser Pro Pro Pro Leu Pro Gln Pro Ser Pro
218 65               70               75               80
219 Pro Ala Pro Thr Thr Pro Gly Ser Pro Pro Ala Pro Val Thr Pro Pro
220               85               90               95
221 Thr Arg Asn Pro Pro Pro Ser Val Pro Gly Pro Pro Ser Asn Pro Ser
222               100               105               110
223 Arg Glu Gly Gly Ser Pro Arg Pro Pro Ser Ser Pro Ser Pro Pro Ser
224               115               120               125
225 Pro Ser Ser Asp Gly Leu Ser Thr Gly Val Val Val Gly Ile Ala Ile
226       130               135               140
227 Gly Gly Val Ala Leu Leu Val Ile Val Thr Leu Ile Cys Leu Leu Cys
228 145               150               155               160
229 Lys Lys Lys Arg Arg Arg Asp Glu Glu Asp Ala Tyr Tyr Val Pro Pro
230               165               170               175
231 Pro Pro Pro Pro Gly Pro Lys Ala Gly Gly Pro Tyr Gly Gly Gln Gln
232               180               185               190
233 Gln Gln Trp Arg Gln Gln Asn Ala Thr Pro Pro Ser Asp His Val Val
234               195               200               205
235 Thr Ser Leu Pro Pro Pro Pro Lys Ala Pro Ser Pro Pro Arg Gln Pro
236       210               215               220
237 Pro Pro Pro Pro Pro Pro Pro Phe Met Ser Ser Ser Gly Gly Ser Asp
238 225               230               235               240
239 Tyr Ser Asp Arg Pro Val Leu Pro Pro Pro Ser Pro Gly Leu Val Leu
240               245               250               255
241 Gly Phe Ser Lys Ser Thr Phe Thr Tyr Glu Glu Leu Ala Arg Ala Thr
242               260               265               270
243 Asn Gly Phe Ser Glu Ala Asn Leu Leu Gly Gln Gly Gly Phe Gly Tyr
244       275               280               285
245 Val His Lys Gly Val Leu Pro Ser Gly Lys Glu Val Ala Val Lys Gln
246       290               295               300
247 Leu Lys Val Gly Ser Gly Gln Gly Glu Arg Glu Phe Gln Ala Glu Val
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248 305                    310                    315                    320
249 Glu Ile Ile Ser Arg Val His His Arg His Leu Val Ser Leu Val Gly
250                325                    330                    335
251 Tyr Cys Ile Ala Gly Ala Lys Arg Leu Leu Val Tyr Glu Phe Val Pro
252                340                    345                    350
253 Asn Asn Asn Leu Glu Leu His Leu His Gly Glu Gly Arg Pro Thr Met
254                355                    360                    365
255 Glu Trp Ser Thr Arg Leu Lys Ile Ala Leu Gly Ser Ala Lys Gly Leu
256        370                    375                    380
257 Ser Tyr Leu His Glu Asp Cys Asn Pro Lys Ile Ile His Arg Asp Ile
258 385                    390                    395                    400
259 Lys Ala Ser Asn Ile Leu Ile Asp Phe Lys Phe Glu Ala Lys Val Ala
260                405                    410                    415
261 Asp Phe Gly Leu Ala Lys Ile Ala Ser Asp Thr Asn Thr His Val Ser
262                420                    425                    430
263 Thr Arg Val Met Gly Thr Phe Gly Tyr Leu Ala Pro Glu Tyr Ala Ala
264                435                    440                    445
265 Ser Gly Lys Leu Thr Glu Lys Ser Asp Val Phe Ser Phe Gly Val Val
266        450                    455                    460
267 Leu Leu Glu Leu Ile Thr Gly Arg Arg Pro Val Asp Ala Asn Asn Val
268 465                    470                    475                    480
269 Tyr Val Asp Asp Ser Leu Val Asp Trp Ala Arg Pro Leu Leu Asn Arg
270                485                    490                    495
271 Ala Ser Glu Gln Gly Asp Phe Glu Gly Leu Ala Asp Ala Lys Met Asn
272                500                    505                    510
273 Asn Gly Tyr Asp Arg Glu Glu Met Ala Arg Met Val Ala Cys Ala Ala
274                515                    520                    525
275 Ala Cys Val Arg His Ser Ala Arg Arg Arg Pro Arg Met Ser Gln Ile
276        530                    535                    540
277 Val Arg Ala Leu Glu Gly Asn Val Ser Leu Ser Asp Leu Asn Glu Gly
278 545                    550                    555                    560
279 Met Arg Pro Gly Gln Ser Asn Val Tyr Ser Ser Tyr Gly Gly Ser Thr
280                565                    570                    575
281 Asp Tyr Asp Ser Ser Gln Tyr Asn Glu Asp Met Lys Lys Phe Arg Lys
282                580                    585                    590
283 Met Ala Leu Gly Thr Gln Glu Tyr Asn Ala Thr Gly Glu Tyr Ser Asn
284        595                    600                    605
285 Pro Thr Ser Asp Tyr Gly Leu Tyr Pro Ser Gly Ser Ser Ser Glu Gly
286        610                    615                    620
287 Gln Thr Thr Arg Glu Met Glu Met Gly Lys Ile Lys Arg Thr Gly Gln
288 625                    630                    635                    640
289 Gly Tyr Ser Gly Pro Ser Leu
290                645
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 2189
295 <212> TYPE: DNA
296 <213> ORGANISM: Brassica napus
300 <220> FEATURE:
301 <221> NAME/KEY: CDS
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 07/23/2002
PATENT APPLICATION: US/10/086,464   TIME: 13:08:24

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF3\07232002\J086464.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 3,12,15,18,21,22,25
Seq#:19; Xaa Pos. 7
Seq#:20; N Pos. 3,6,8,9,15,18,21,22
Seq#:23; N Pos. 2,3,5,6,9,12,14,15,18,21

VERIFICATION SUMMARY   DATE: 07/23/2002
PATENT APPLICATION: US/10/086,464   TIME: 13:08:24

Input Set : **A:\Sequence Listing.txt**
Output Set: **N:\CRF3\07232002\J086464.raw**

L:310 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 3, CDS LOCATION:1..2189
L:2086 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:2100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
L:2118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:0
L:2158 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0